

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/647,544A

Source: 1FW/6

Date Processed by STIC: 6/24/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 06/24/2005

PATENT APPLICATION: US/09/647,544A

TIME: 10:05:20

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Output Set: N:\CRF4\06242005\I647544A.raw

3 <110> APPLICANT: LUNDGREN-AKERLUND, EVY
 5 <120> TITLE OF INVENTION: INTEGRIN HETERODIMER AND A SUBUNIT THEREOF
 7 <130> FILE REFERENCE: 034341-001
 9 <140> CURRENT APPLICATION NUMBER: 09/647,544A
 10 <141> CURRENT FILING DATE: 2000-10-26
 12 <150> PRIOR APPLICATION NUMBER: PCT/SE99/00544
 13 <151> PRIOR FILING DATE: 1999-03-31
 15 <150> PRIOR APPLICATION NUMBER: SE 9900319.6
 16 <151> PRIOR FILING DATE: 1999-01-28
 18 <150> PRIOR APPLICATION NUMBER: SE 9801164-6
 19 <151> PRIOR FILING DATE: 1998-04-02
 21 <160> NUMBER OF SEQ ID NOS: 299
 23 <170> SOFTWARE: PatentIn Ver. 3.3
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 3884
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (22)..(3522)
 34 <400> SEQUENCE: 1

pp 6-7

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36	Met Glu Leu Pro Phe Val Thr His Leu Phe	
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39	ttg ccc ctg gtg ttc ctg aca ggt ctc tgc tcc ccc ttt aac ctg gat	99
40	Leu Pro Leu Val Phe Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp	
41	15 20 25	
43	gaa cat cac cca cgc cta ttc cca ggg cca cca gaa gct gaa ttt gga	147
44	Glu His His Pro Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly	
45	30 35 40	
47	tac agt gtc tta caa cat gtt ggg ggt gga cag cga tgg atg ctg gtg	195
48	Tyr Ser Val Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val	
49	45 50 55	
51	ggc gcc ccc tgg gat ggg cct tca ggc gac cgg agg ggg gac gtt tat	243
52	Gly Ala Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr	
53	60 65 70	
55	cgc tgc cct gta ggg ggg gcc cac aat gcc cca tgt gcc aag ggc cac	291
56	Arg Cys Pro Val Gly Ala His Asn Ala Pro Cys Ala Lys Gly His	
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59	tta ggt gac tac caa ctg gga aat tca tct cat cct gct gtg aat atg	339
60	Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn Met	
61	95 100 105	
63	cac ctg ggg atg tct ctg tta gag aca gat ggt gat ggg gga ttc atg	387

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68 Ala Cys Ala Pro Leu Trp Ser Arg Ala Cys Gly Ser Ser Val Phe Ser
69          125          130          135
71 tct ggg ata tgt gcc cgt gtg gat gct tca ttc cag cct cag gga agc 483
72 Ser Gly Ile Cys Ala Arg Val Asp Ala Ser Phe Gln Pro Gln Gly Ser
73          140          145          150
75 ctg gca ccc act gcc caa cgc tgc cca aca tac atg gat gtt gtc att 531
76 Leu Ala Pro Thr Ala Gln Arg Cys Pro Thr Tyr Met Asp Val Val Ile
77 155          160          165          170
79 gtc ttg gat ggc tcc aac agc atc tac ccc tgg tct gaa gtt cag acc 579
80 Val Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Ser Glu Val Gln Thr
81          175          180          185
83 ttc cta cga aga ctg gta ggg aaa ctg ttt att gac cca gaa cag ata 627
84 Phe Leu Arg Arg Leu Val Gly Lys Leu Phe Ile Asp Pro Glu Gln Ile
85          190          195          200
87 cag gtg gga ctg gta cag tat ggg gag agc cct gta cat gag tgg tcc 675
88 Gln Val Gly Leu Val Gln Tyr Gly Glu Ser Pro Val His Glu Trp Ser
89          205          210          215
91 ctg gga gat ttc cga acg aag gaa gaa gtg gtg aga gca gca aag aac 723
92 Leu Gly Asp Phe Arg Thr Lys Glu Glu Val Val Arg Ala Ala Lys Asn
93          220          225          230
95 ctc agt cgg cgg gag gga cga gaa aca aag act gcc caa gca ata atg 771
96 Leu Ser Arg Arg Glu Gly Arg Glu Thr Lys Thr Ala Gln Ala Ile Met
97 235          240          245          250
99 gtg gcc tgc aca gaa ggg ttc agt cag tcc cat ggg ggc cga ccc gag 819
100 Val Ala Cys Thr Glu Gly Phe Ser Gln Ser His Gly Gly Arg Pro Glu
101          255          260          265
103 gct gcc agg cta ctg gtg gtt gtc act gat gga gag tcc cat gat gga 867
104 Ala Ala Arg Leu Leu Val Val Val Thr Asp Gly Glu Ser His Asp Gly
105          270          275          280
107 gag gag ctt cct gca gca cta aag gcc tgt gag gct gga aga gtg aca 915
108 Glu Glu Leu Pro Ala Ala Leu Lys Ala Cys Glu Ala Gly Arg Val Thr
109          285          290          295
111 cgc tat ggg att gca gtc ctt ggt cac tac ctc cgg cgg cag cga gat 963
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116 Pro Ser Ser Phe Leu Arg Glu Ile Arg Thr Ile Ala Ser Asp Pro Asp
117 315          320          325          330
119 gag cga ttc ttc ttc aat gtc aca gat gag gct gct ctg act gac att 1059
120 Glu Arg Phe Phe Phe Asn Val Thr Asp Glu Ala Ala Leu Thr Asp Ile
121          335          340          345
123 gtg gat gca cta gga gat cgg att ttt ggc ctt gaa ggg tcc cat gca 1107
124 Val Asp Ala Leu Gly Asp Arg Ile Phe Gly Leu Glu Gly Ser His Ala
125          350          355          360
127 gaa aac gaa agc tcc ttt ggg ctg gaa atg tct cag att ggt ttc tcc 1155
128 Glu Asn Glu Ser Ser Phe Gly Leu Glu Met Ser Gln Ile Gly Phe Ser

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132 Thr His Arg Leu Lys Asp Gly Ile Leu Phe Gly Met Val Gly Ala Tyr
133          380          385          390
135 gac tgg gga ggc tct gtg cta tgg ctt gaa gga ggc cac cgc ctt ttc 1251
136 Asp Trp Gly Gly Ser Val Leu Trp Leu Glu Gly Gly His Arg Leu Phe
137 395          400          405          410
139 ccc cca cga atg gca ctg gaa gac gag ttc ccc cct gca ctg cag aac 1299
140 Pro Pro Arg Met Ala Leu Glu Asp Glu Phe Pro Pro Ala Leu Gln Asn
141          415          420          425
143 cat gca gcc tac ctg ggt tac tct gtt tct tcc atg ctt ttg cgg ggt 1347
144 His Ala Ala Tyr Leu Gly Tyr Ser Val Ser Ser Met Leu Leu Arg Gly
145          430          435          440
147 gga cgc cgc ctg ttt ctc tct ggg gct cct cga ttt aga cat cga gga 1395
148 Gly Arg Arg Leu Phe Leu Ser Gly Ala Pro Arg Phe Arg His Arg Gly
149          445          450          455
151 aaa gtc atc gcc ttc cag ctt aag aaa gat ggg gct gtg agg gtt gcc 1443
152 Lys Val Ile Ala Phe Gln Leu Lys Lys Asp Gly Ala Val Arg Val Ala
153          460          465          470
155 cag agc ctc cag ggg gag cag att ggt tca tac ttt ggc agt gag ctc 1491
156 Gln Ser Leu Gln Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Glu Leu
157 475          480          485          490
159 tgc cca ttg gat aca gat agg gat gga aca act gat gtc tta ctt gtg 1539
160 Cys Pro Leu Asp Thr Asp Arg Asp Gly Thr Thr Asp Val Leu Leu Val
161          495          500          505
163 gct gcc ccc atg ttc ctg gga ccc cag aac aag gaa aca gga cgt gtt 1587
164 Ala Ala Pro Met Phe Leu Gly Pro Gln Asn Lys Glu Thr Gly Arg Val
165          510          515          520
167 tat gtg tat ctg gta ggc cag cag tcc ttg ctg acc ctc caa gga aca 1635
168 Tyr Val Tyr Leu Val Gly Gln Gln Ser Leu Leu Thr Leu Gln Gly Thr
169          525          530          535
171 ctt cag cca gaa ccc ccc cag gat gct cgg ttt ggc ttt gcc atg gga 1683
172 Leu Gln Pro Glu Pro Pro Gln Asp Ala Arg Phe Gly Phe Ala Met Gly
173          540          545          550
175 gct ctt cct gat ctg aac caa gat ggt ttt gct gat gtg gct gtg ggg 1731
176 Ala Leu Pro Asp Leu Asn Gln Asp Gly Phe Ala Asp Val Ala Val Gly
177 555          560          565          570
179 gcg cct ctg gaa gat ggg cac cag gga gca ctg tac ctg tac cat gga 1779
180 Ala Pro Leu Glu Asp Gly His Gln Gly Ala Leu Tyr Leu Tyr His Gly
181          575          580          585
183 acc cag agt gga gtc agg ccc cat cct gcc cag agg att gct gct gcc 1827
184 Thr Gln Ser Gly Val Arg Pro His Pro Ala Gln Arg Ile Ala Ala Ala
185          590          595          600
187 tcc atg cca cat gcc ctc agc tac ttt ggc cga agt gtg gat ggt cgg 1875
188 Ser Met Pro His Ala Leu Ser Tyr Phe Gly Arg Ser Val Asp Gly Arg
189          605          610          615
191 cta gat ctg gat gga gat gat ctg gtc gat gtg gct gtg ggt gcc cag 1923
192 Leu Asp Leu Asp Gly Asp Asp Leu Val Asp Val Ala Val Gly Ala Gln
193          620          625          630

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196	Gly Ala Ala Ile Leu Leu Ser Ser Arg Pro Ile Val His Leu Thr Pro	
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199	tca ctg gag gtg acc cca cag gcc atc agt gtg gtt cag agg gac tgt	2019
200	Ser Leu Glu Val Thr Pro Gln Ala Ile Ser Val Val Gln Arg Asp Cys	
201	655 660 665	
203	agg cgg cga ggc caa gaa gca gtc tgt ctg act gca gcc ctt tgc ttc	2067
204	Arg Arg Arg Gly Gln Glu Ala Val Cys Leu Thr Ala Ala Leu Cys Phe	
205	670 675 680	
207	caa gtg acc tcc cgt act cct ggt cgc tgg gat cac caa ttc tac atg	2115
208	Gln Val Thr Ser Arg Thr Pro Gly Arg Trp Asp His Gln Phe Tyr Met	
209	685 690 695	
211	agg ttc acc gca tca ctg gat gaa tgg act gct ggg gca cgt gca gca	2163
212	Arg Phe Thr Ala Ser Leu Asp Glu Trp Thr Ala Gly Ala Arg Ala Ala	
213	700 705 710	
215	ttt gat ggc tct ggc cag agg ttg tcc cct cgg agg ctc cgg ctc agt	2211
216	Phe Asp Gly Ser Gly Gln Arg Leu Ser Pro Arg Arg Leu Arg Leu Ser	
217	715 720 725 730	
219	gtg ggg aat gtc act tgt gag cag cta cac ttc cat gtg ctg gat aca	2259
220	Val Gly Asn Val Thr Cys Glu Gln Leu His Phe His Val Leu Asp Thr	
221	735 740 745	
223	tca gat tac ctc cgg cca gtg gcc ttg act gtg acc ttt gcc ttg gac	2307
224	Ser Asp Tyr Leu Arg Pro Val Ala Leu Thr Val Thr Phe Ala Leu Asp	
225	750 755 760	
227	aat act aca aag cca ggg cct gtg ctg aat gag ggc tca ccc acc tct	2355
228	Asn Thr Thr Lys Pro Gly Pro Val Leu Asn Glu Gly Ser Pro Thr Ser	
229	765 770 775	
231	ata caa aag ctg gtc ccc ttc tca aag gat tgt ggc cct gac aat gaa	2403
232	Ile Gln Lys Leu Val Pro Phe Ser Lys Asp Cys Gly Pro Asp Asn Glu	
233	780 785 790	
235	tgt gtc aca gac ctg gtg ctt caa gtg aat atg gac atc aga ggc tcc	2451
236	Cys Val Thr Asp Leu Val Leu Gln Val Asn Met Asp Ile Arg Gly Ser	
237	795 800 805 810	
239	agg aag gcc cca ttt gtg gtt cga ggt ggc cgg cgg aaa gtg ctg gta	2499
240	Arg Lys Ala Pro Phe Val Val Arg Gly Gly Arg Arg Lys Val Leu Val	
241	815 820 825	
243	tct aca act ctg gag aac aga aag gaa aat gct tac aat acg agc ctg	2547
244	Ser Thr Thr Leu Glu Asn Arg Lys Glu Asn Ala Tyr Asn Thr Ser Leu	
245	830 835 840	
247	agt atc atc ttc tct aga aac ctc cac ctg gcc agt ctc act cct cag	2595
248	Ser Ile Ile Phe Ser Arg Asn Leu His Leu Ala Ser Leu Thr Pro Gln	
249	845 850 855	
251	aga gag agc cca ata aag gtg gaa tgt gcc gcc cct tct gct cat gcc	2643
252	Arg Glu Ser Pro Ile Lys Val Glu Cys Ala Ala Pro Ser Ala His Ala	
253	860 865 870	
255	cgg ctc tgc agt gtg ggg cat cct gtc ttc cag act gga gcc aag gtg	2691
256	Arg Leu Cys Ser Val Gly His Pro Val Phe Gln Thr Gly Ala Lys Val	
257	875 880 885 890	
259	acc ttt ctg cta gag ttt gag ttt agc tgc tcc tct ctc ctg agc cag	2739

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261					895					900					905		
263	gtc	ttt	ggg	aag	ctg	act	gcc	agc	agt	gac	agc	ctg	gag	aga	aat	ggc	2787
264	Val	Phe	Gly	Lys	Leu	Thr	Ala	Ser	Ser	Asp	Ser	Leu	Glu	Arg	Asn	Gly	
265				910					915					920			
267	acc	ctt	caa	gaa	aac	aca	gcc	cag	acc	tca	gcc	tac	atc	caa	tat	gag	2835
268	Thr	Leu	Gln	Glu	Asn	Thr	Ala	Gln	Thr	Ser	Ala	Tyr	Ile	Gln	Tyr	Glu	
269			925					930					935				
271	ccc	cac	ctc	ctg	ttc	tct	agt	gag	tct	acc	ctg	cac	cgc	tat	gag	gtt	2883
272	Pro	His	Leu	Leu	Phe	Ser	Ser	Glu	Ser	Thr	Leu	His	Arg	Tyr	Glu	Val	
273		940					945					950					
275	cac	cca	tat	ggg	acc	ctc	cca	gtg	ggt	cct	ggc	cca	gaa	ttc	aaa	acc	2931
276	His	Pro	Tyr	Gly	Thr	Leu	Pro	Val	Gly	Pro	Gly	Pro	Glu	Phe	Lys	Thr	
277	955					960					965				970		
279	act	ctc	agg	gtt	cag	aac	cta	ggc	tgc	tat	gtg	gtc	agt	ggc	ctc	atc	2979
280	Thr	Leu	Arg	Val	Gln	Asn	Leu	Gly	Cys	Tyr	Val	Val	Ser	Gly	Leu	Ile	
281				975					980					985			
283	atc	tca	gcc	ctc	ctt	cca	gct	gtg	gcc	cat	ggg	ggc	aat	tac	ttc	cta	3027
284	Ile	Ser	Ala	Leu	Leu	Pro	Ala	Val	Ala	His	Gly	Gly	Asn	Tyr	Phe	Leu	
285				990					995					1000			
287	tca	ctg	tct	caa	gtc	atc	act	aac	aat	gca	agc	tgc	ata	gtg	cag	aac	3075
288	Ser	Leu	Ser	Gln	Val	Ile	Thr	Asn	Asn	Ala	Ser	Cys	Ile	Val	Gln	Asn	
289			1005					1010					1015				
291	ctg	act	gaa	ccc	cca	ggc	cca	cct	gtg	cat	cca	gag	gag	ctt	caa	cac	3123
292	Leu	Thr	Glu	Pro	Pro	Gly	Pro	Pro	Val	His	Pro	Glu	Glu	Leu	Gln	His	
293		1020					1025					1030					
295	aca	aac	aga	ctg	aat	ggg	agc	aat	act	cag	tgt	cag	gtg	gtg	agg	tgc	3171
296	Thr	Asn	Arg	Leu	Asn	Gly	Ser	Asn	Thr	Gln	Cys	Gln	Val	Val	Arg	Cys	
297	1035				1040					1045					1050		
299	cac	ctt	ggg	cag	ctg	gca	aag	ggg	act	gag	gtc	tct	gtt	gga	cta	ttg	3219
300	His	Leu	Gly	Gln	Leu	Ala	Lys	Gly	Thr	Glu	Val	Ser	Val	Gly	Leu	Leu	
301				1055					1060					1065			
303	agg	ctg	gtt	cac	aat	gaa	ttt	ttc	cga	aga	gcc	aag	ttc	aag	tcc	ctg	3267
304	Arg	Leu	Val	His	Asn	Glu	Phe	Phe	Arg	Arg	Ala	Lys	Phe	Lys	Ser	Leu	
305				1070					1075					1080			
307	acg	gtg	gtc	agc	acc	ttt	gag	ctg	gga	acc	gaa	gag	ggc	agt	gtc	cta	3315
308	Thr	Val	Val	Ser	Thr	Phe	Glu	Leu	Gly	Thr	Glu	Glu	Gly	Ser	Val	Leu	
309			1085					1090					1095				
311	cag	ctg	act	gaa	gcc	tcc	cgt	tgg	agt	gag	agc	ctc	ttg	gag	gtg	gtt	3363
312	Gln	Leu	Thr	Glu	Ala	Ser	Arg	Trp	Ser	Glu	Ser	Leu	Leu	Glu	Val	Val	
313		1100					1105					1110					
315	cag	acc	cgg	cct	atc	ctc	atc	tcc	ctg	tgg	atc	ctc	ata	ggc	agt	gtc	3411
316	Gln	Thr	Arg	Pro	Ile	Leu	Ile	Ser	Leu	Trp	Ile	Leu	Ile	Gly	Ser	Val	
317	1115				1120					1125					1130		
319	ctg	gga	ggg	ttg	ctc	ctg	ctt	gct	ctc	ctt	gtc	ttc	tgc	ctg	tgg	aag	3459
320	Leu	Gly	Gly	Leu	Leu	Leu	Leu	Ala	Leu	Val	Phe	Cys	Leu	Trp	Lys		
321				1135					1140					1145			
323	ctt	ggc	ttc	ttt	gcc	cat	aag	aaa	atc	cct	gag	gaa	gaa	aaa	aga	gaa	3507
324	Leu	Gly	Phe	Phe	Ala	His	Lys	Lys	Ile	Pro	Glu	Glu	Glu	Lys	Arg	Glu	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:11; N Pos. 2,5,14
Seq#:15; N Pos. 1,13,16
Seq#:22; Xaa Pos. 2,6
Seq#:24; Xaa Pos. 2
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Seq#:33; Xaa Pos. 1,2,3,4,6,7,8,10,12,13,14,16,18,19,21,25,28,30,31,33,34
Seq#:33; Xaa Pos. 35,36,40,41,43,44,46,47,49,51,54,55,56,59,61,66,70,72,75
Seq#:33; Xaa Pos. 76,78
Seq#:34; Xaa Pos. 1,3,4,6,8,11,13,16,18,20
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Seq#:43; Xaa Pos. 3
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Seq#:130; Xaa Pos. 42,47,48,49,54,55,58,65,66,69,70,71,73,74,76,80,82,83,84
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Seq#:209; Xaa Pos. 42,43,47,48,49,54,56,58,59,60,61,62,63,65,66,69,71,72,73
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Seq#:212; Xaa Pos. 1
Seq#:213; Xaa Pos. 6,8,14,20,21
Seq#:214; Xaa Pos. 10
Seq#:216; Xaa Pos. 20,25,33,37
Seq#:219; Xaa Pos. 1
Seq#:221; Xaa Pos. 3,7

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Input Set : A:\34341001.app
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Seq#:222; Xaa Pos. 49
Seq#:245; Xaa Pos. 37
Seq#:247; Xaa Pos. 9

VERIFICATION SUMMARY

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Input Set : A:\34341001.app

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L:1293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:1397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:1430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:1508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:1639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
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L:2033 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
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M:341 Repeated in SeqNo=34
L:2145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:2175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:2231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
M:341 Repeated in SeqNo=37
L:2255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:2292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
M:341 Repeated in SeqNo=39
L:2320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:2340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:16
L:2376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
M:341 Repeated in SeqNo=42
L:2412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:3642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:0
M:341 Repeated in SeqNo=128
L:3703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129 after pos.:0
M:341 Repeated in SeqNo=129
L:3843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130 after pos.:0
M:341 Repeated in SeqNo=130
L:3883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:0
L:3900 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132 after pos.:0
L:3920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133 after pos.:0
L:3996 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134 after pos.:0
M:341 Repeated in SeqNo=134
L:4304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:150 after pos.:48
M:341 Repeated in SeqNo=150
L:5185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:207 after pos.:0
L:5211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:208 after pos.:0
L:5358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:209 after pos.:0
M:341 Repeated in SeqNo=209
L:5414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:210 after pos.:0
L:5435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:211 after pos.:0
L:5451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:212 after pos.:0
L:5486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:213 after pos.:0
M:341 Repeated in SeqNo=213
L:5506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:214 after pos.:0
L:5551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:16

VERIFICATION SUMMARY

DATE: 06/24/2005

PATENT APPLICATION: US/09/647,544A

TIME: 10:05:21

Input Set : A:\34341001.app

Output Set: N:\CRF4\06242005\I647544A.raw

M:341 Repeated in SeqNo=216

L:5599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:219 after pos.:0